Case Study

Predict High-Risk Donors for Hepatitis C:

Predict high risk donors using the ‘K-Nearest Neighbors’ model

KNN 모델을 활용한 HCV 고위험 헌혈자 선별

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Background & Objective

Background

- Hepatitis C Virus(HCV) is known to be a ‘transfusion-transmissible infections(TTI)’
- World Health Organization(WHO) recommends all blood donations should be screened for HCV*
- Predicting donors with a high-risk of Hepatitis C (before testing HCV) will help blood centers to pre-screen and monitor high-risk donors, enhancing blood safety.

** WHO, Blood safety and availability*

Objective

- Predict blood donor with a high risk of Hepatitis C
- Identify which variables have an impact on classifying Hepatitis C patient

Pace : Plan Stage

Plan (Data Collection & Preprocessing)

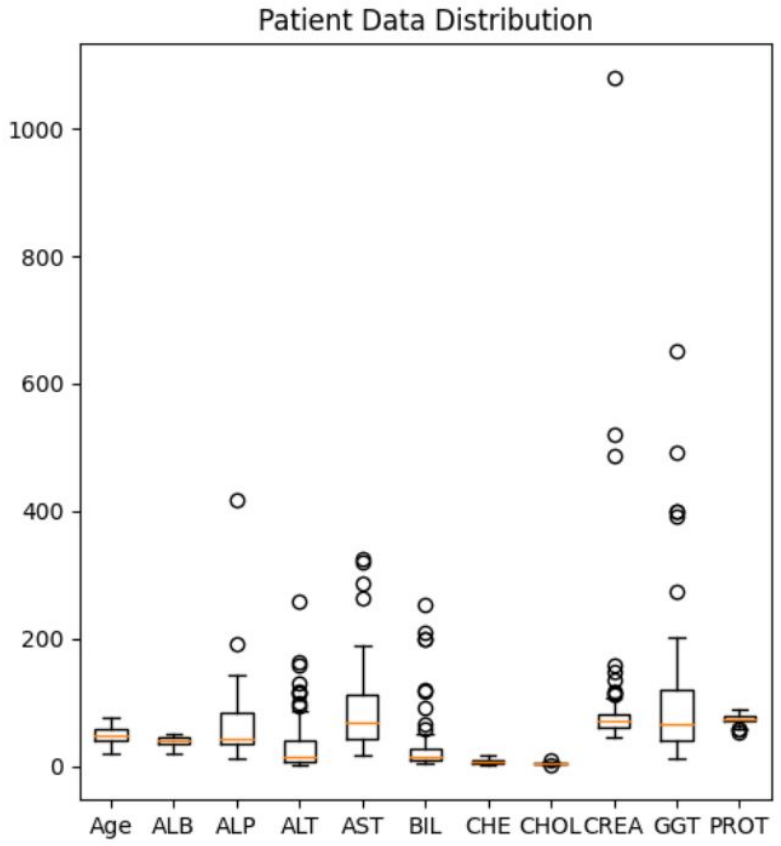
- Data Collection
  - Data from UCI Machine Learning Repository*
  - Data has 615 people data including 7 blood test results
    - Blood Test Items: 'ALB', 'ALP', 'ALT', 'AST', 'BIL', 'CHE', 'CHOL', 'CREA', 'GGT', 'PROT'
  - Target attribute has 4 types of categories: blood donors, hepatitis C, fibrosis, and Cirrhosis
- Pre-processing
  - Replaced 31 missing values with the group mean of each category.
  - Merged all Hepatitis C patient's data into one category; 'patient'
  - Excluded 'suspect blood donor' data from modeling for final test (prevent data leakage)

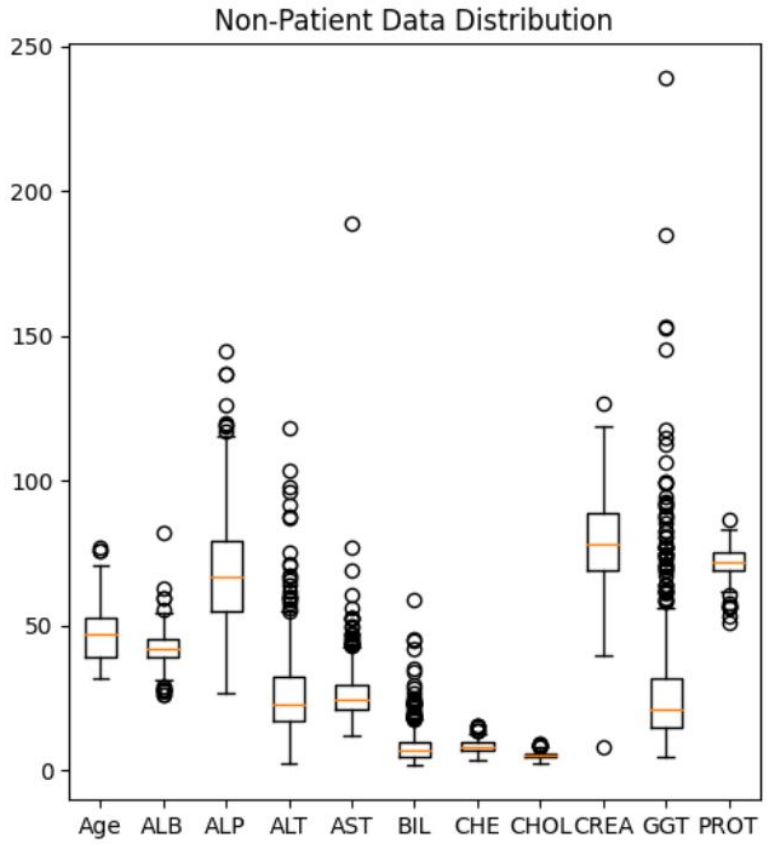
* Lichtinghagen,Ralf, Klawonn,Frank, and Hoffmann,Georg. (2020). HCV data. UCI Machine Learning Repository. https://doi.org/10.24432/C5D612.

pAce: Analyze Stage

Data Distribution

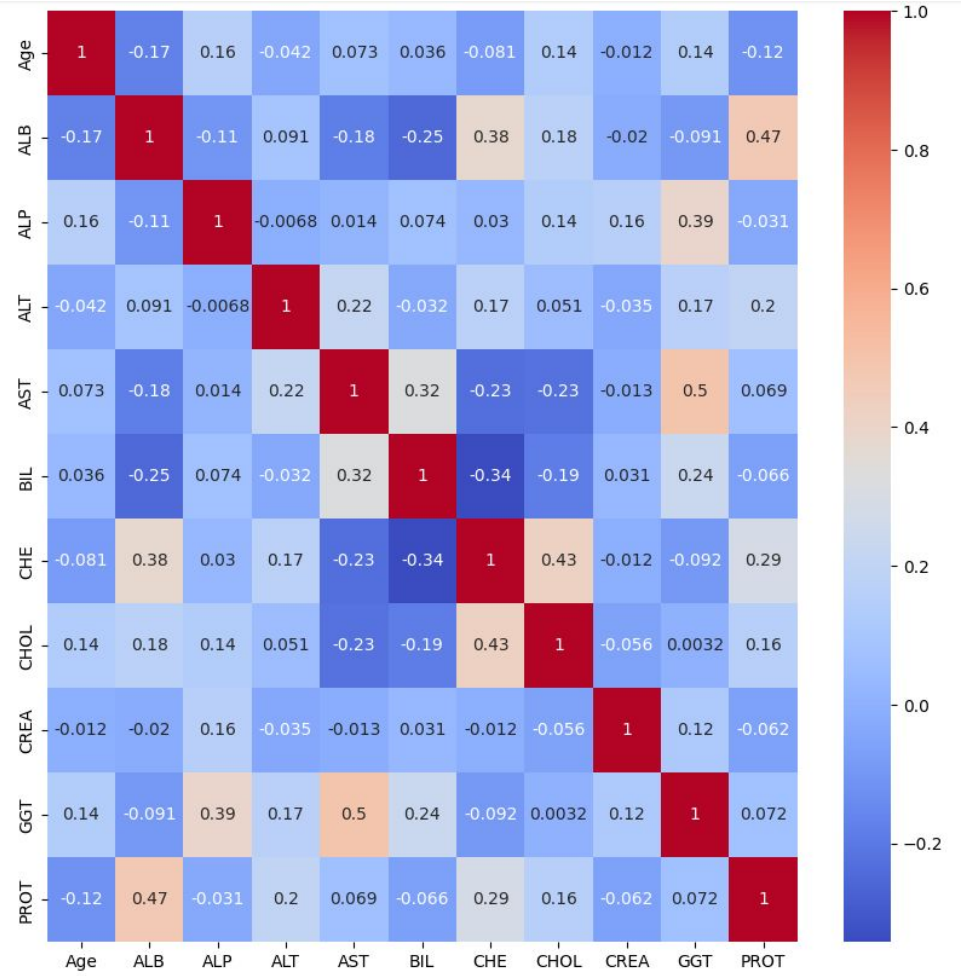
- Identified outliers across blood test items
  → Removed outliers(using Z score) on selected items considering the characteristic of the KNN model
  → Scaled data before training





Relationship between features

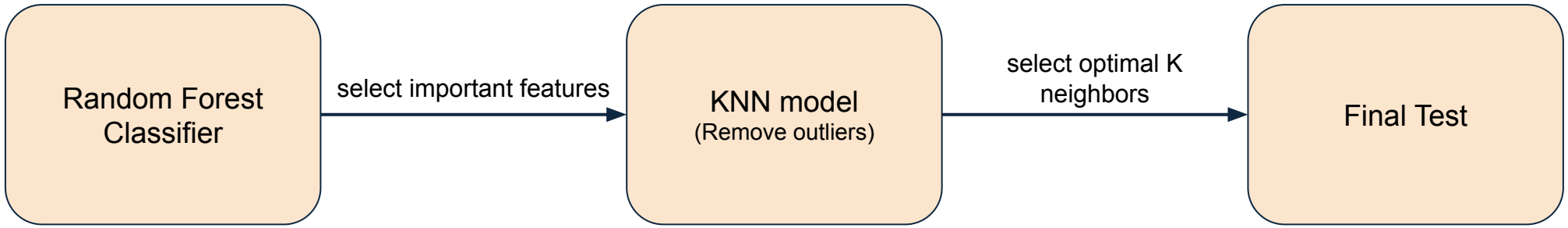
- Identified there are some correlations between variables.
  - PROT - ALB
  - GGT - AST
  - CHE - CHOL
- To prevent dimensionality reduction and overfitting, used a random forest model to find important features



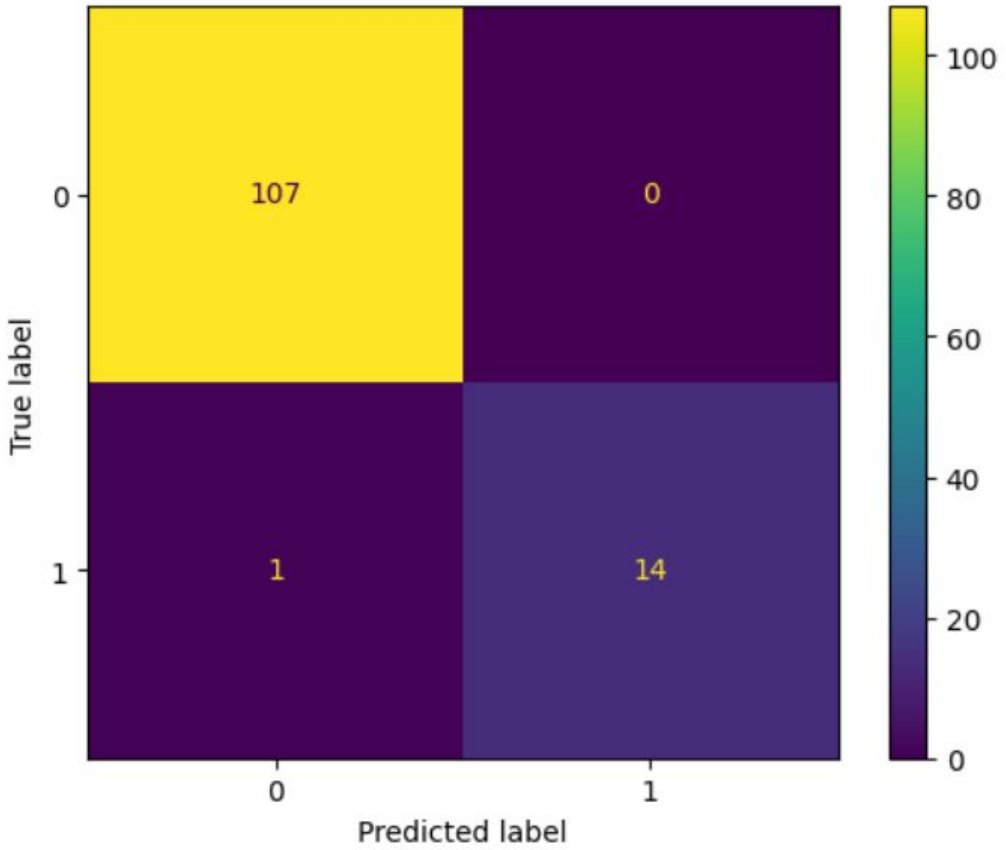
paCe: Construct Stage

Prepare Modeling

- The goal of this study is to classify(and predict) Hepatitis C patient
- To select important features, used a Random Forest Classifier, then built a K-NN model using selected features
- The KNN model is a simple algorithm with fewer parameters to adjust. The model is capable of classifying with small datasets and high dimensionality.
- Due to the class imbalance, used undersampling and SMOTE method (80% non-patient : 20% patient)
  a. selected F1 score as the main evaluation score
- Used 'suspect blood donor' category data to predict if the donor has a high-risk of hepatitis C



Model Results(Random Forest Classifier)



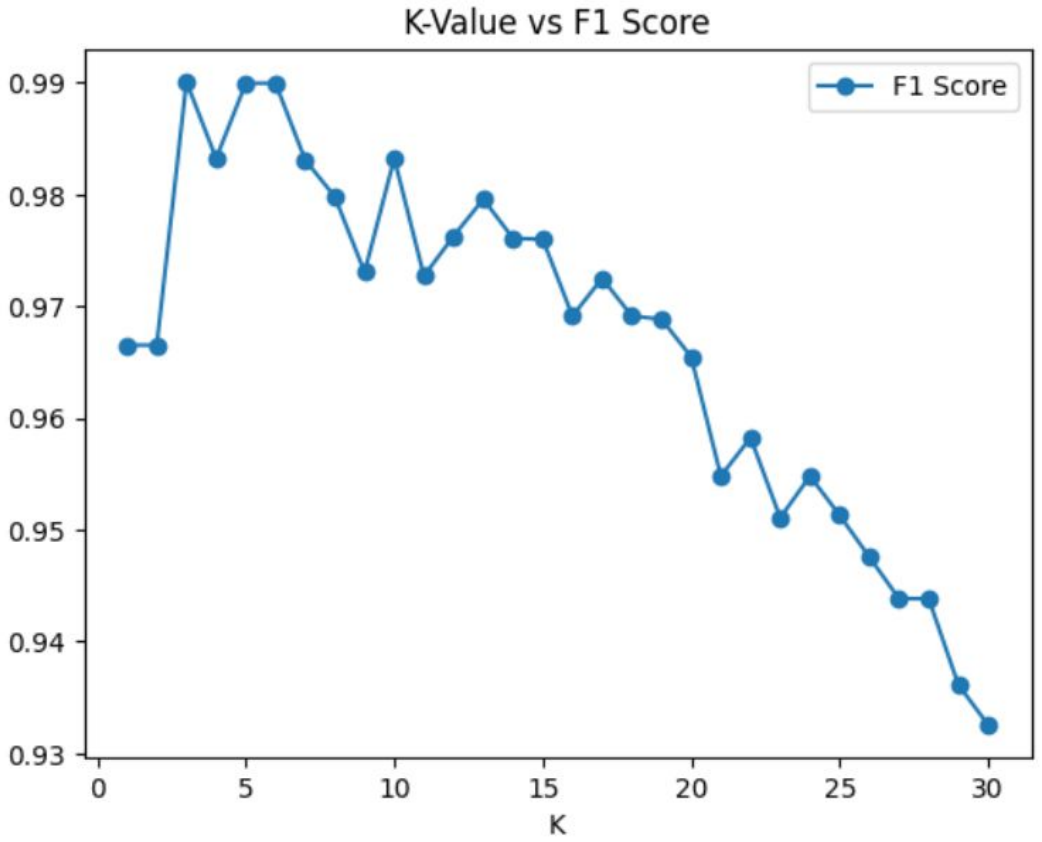
	Feature	Importance
0	AST	0.387839
1	GGT	0.175390
2	BIL	0.123582
3	ALP	0.121319
4	ALT	0.061418

- From the Random Forest model, able to extract top important features with high evaluation score
  - Important features: AST, GGT, BIL, ALP, ALT
  - F1 score: 0.96
    Accuracy score: 0.99
    ROC score: 0.96
- Added two additional features(ALB, CHOL), considering current testing items at the blood center

Construct Model

Target (y)	Patient (1, 0) → 20%(1) : 80%(0)
Feature (X)	AST, GGT, BIL, ALP, ALT, ALB, CHOL *Removed outliers by each target class
Model	K-Nearest Neighbor(KNN) Model
Scaling	Downsampling → SMOTE (Upsampling) → Standard Scaler
Evaluation	F1 score, Accuracy score, and ROC score

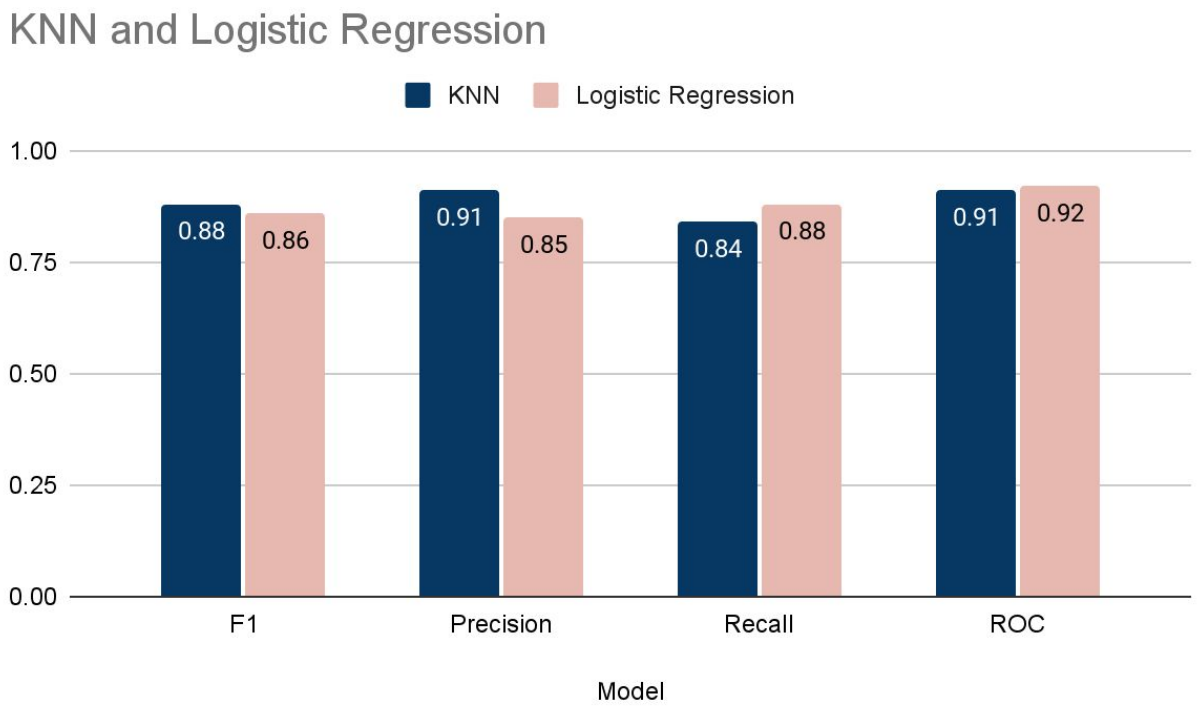
KNN Model Results



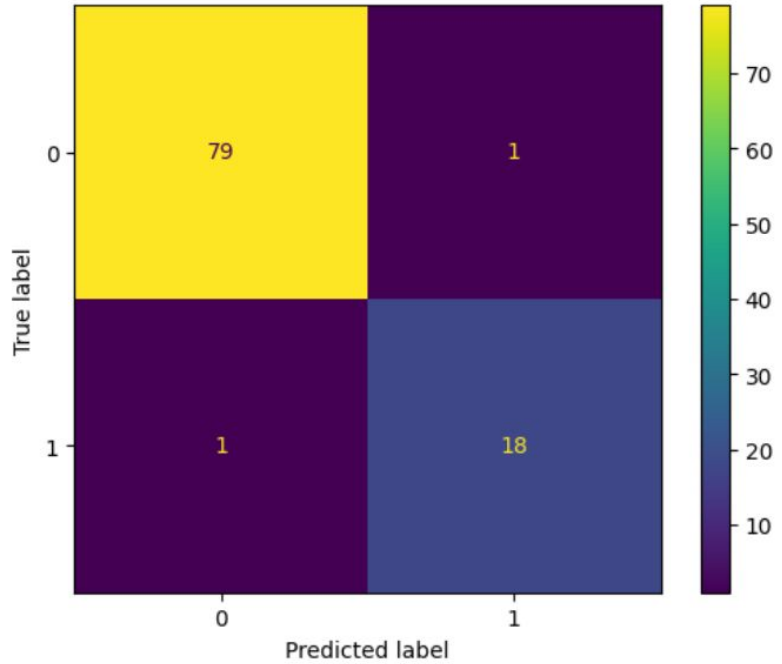
	K	F1 Score
2	3	0.990097
4	5	0.989966
6	7	0.983094
12	13	0.979588
14	15	0.976008

- Found K values of 3, 5, and 7 showed highest F1 score of 0.96
- To prevent 'overfitting' and 'underfitting', chose K values of 3 as an optimal k value

Final Model - KNN model with 3 neighbors



<KNN Model Confusion Matrix>



- In the test data, the KNN model showed a higher score of F1 and Precision
- With an ROC score of 0.91, the KNN model performs better than random guessing 91% of the time.
  → Strong ability to classify between the two classes

pacE: Execute Stage

Predict New Dataset

Suspected Blood Donors

	Category	Age	Sex	ALB	ALP	ALT	AST	BIL	CHE	CHOL	CREA	GGT	PROT
534	4	47	m	22.5	124.0	79.5	46.7	2.3	6.83	4.30	170.0	345.6	58.6
535	4	48	m	24.9	116.9	49.2	24.3	4.9	3.44	5.25	29.0	83.0	47.8
536	4	49	m	21.6	42.2	9.5	10.6	2.4	3.75	3.01	64.0	38.9	44.8
537	4	55	m	47.3	106.0	208.8	130.6	0.8	14.80	8.08	76.0	71.6	78.3
538	4	71	m	14.9	69.8	19.7	95.2	9.8	13.30	2.61	9.0	7.6	47.0
539	4	74	m	20.3	84.0	22.8	43.0	5.7	4.91	3.19	52.0	218.3	47.8
540	4	59	f	19.3	208.2	325.3	146.6	6.9	5.33	4.72	32.0	295.6	53.1

```
prediction = optimal_knn_model.predict(new_df_scaled)
print(f'Predicted class for the suspect blood donors : {prediction}')
```

```
Predicted class for the suspect blood donors : [1 1 1 1 1 1 1]
```

Predicted all donors have high risk of HCV

Further investigate these donors' blood samples to prevent any adverse event

Conclusion

- Identified AST, GGT, BIL, ALP, and ALT are important features in predicting HCV
- The KNN model achieved an F1-score of 88%, precision of 91%, and AUC-score of 91% on the test set.
- The KNN model is a simple and effective machine learning model to classify the target in a short time with fewer parameters to be tuned.
- Blood centers can utilize this model to classify donors with a high risk of HCV, enhancing blood safety.
  - If the donor is predicted to have a risk of HCV, further investigate his/her previous blood sample and monitor the next blood donation result

Thank You

Reference

Full Project Code: Github

<Contributions>

- **Yoojin (Audrey) Jung** - Data Analyst (Professional)
  - **(Contribution) EDA (processing & visualization)**
  - (Skills) Data Analytics, Visualization (Tableau), SQL, R, Python
  - (LinkedIn) https://www.linkedin.com/in/yoojin-jung/

- **Hyunjin (Austin) Kang** - Data Scientist (Associate)
  - **(Contribution) Data collection, EDA (feature engineering), construct model**
  - (Interest Area) Public Health
  - (Skills) Machine Learning, Python, SQL
  - (LinkedIn) www.linkedin.com/in/austinkang0702